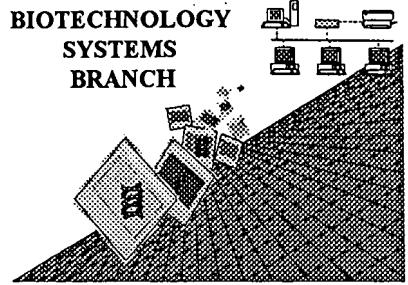


S. Turner

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/183,972

Art Unit / Team No.: 1644

Date Processed by STIC: 2/19/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/183972

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

S. Turner

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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/183,972

DATE: 02/17/2000
TIME: 13:02:25

Input Set: I183972.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

1 <110> Hageman, Gregory S.
2 Kuehn, Markus H.
3 <120> THERAPEUTICS AND DIAGNOSTICS FOR OCULAR DISEASE BASED
4 ON A NOVEL HUMAN GENE FAMILY
5 <130> UIA-027.01
6 <140> US/09/183,972
7 <141> 1998-10-29
E--> OK 8 <160> 49
9 <170> PatentIn Ver. 2.0

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

10 <210> 44
E--> OK 11 <211> 20
12 <212> DNA
13 <213> Artificial Sequence
14 <220>
15 <223> Description of Artificial Sequence: primer
16 delete period ~~400~~ 44
17 ~~period~~ taaaacccca aatgcaatca 20
18 <220>
19 <223> Description of Artificial Sequence: primer
20 <400> 45
E--> OK 21 gcaggctct ctaaacgcat g 21

E--> OK 22 <210> 46
23 <211> 15
24 <212> PRT
25 <213> Homo sapiens
26 <220>
27 <221> UNSURE
28 <222> (1)..(15)
29 <223> applicants are unsure of residues designated as
30 "Xaa" at positions 1 & 11
31 <400> 46
W--> 32 Xaa Ala Leu Phe Pro Asn Gly Val Leu Ile Xaa Pro Xaa Glu Val
33 1 5 10 15

what about Xaa at
position 13? all Xaa's
must
be explained.

See following page for more error

Input Set: I183972.RAW

45 gac acc aag atg cct aca aca gaa aga gaa aca gaa ctc gct gtg tct 480
 46 Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
 47 145 150 155 160
 48 gag gag cag agg gtg gag ctc agc atc tct ctg ata aac cag agg ttc 528
 49 Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
 50 165 170 175
 51 aag gca gag ctc gct gac tct cag tca 555
 52 Lys Ala Glu Leu Ala Asp Ser Gln Ser
 53 180 185
 54 <210> SEQ ID NO 2
 55 <211> LENGTH: 185
 56 <212> TYPE: PRT
 57 <213> ORGANISM: Callimico sp.
 58 <400> SEQUENCE: 2
 59 Ile Phe Phe Pro Asn Gly Val Lys Val Cys Pro Gln Glu Ser Met Lys
 60 1 5 10 15
 61 Gln Ile Leu Ala Ser Leu Gln Ala Tyr Tyr Arg Leu Arg Val Cys Gln
 62 20 25 30
 63 Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp
 64 35 40 45
 65 Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe
 66 50 55 60
 67 Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu
 68 65 70 75 80
 69 Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys
 70 85 90 95
 71 Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile
 72 100 105 110
 73 Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val
 74 115 120 125
 75 Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn
 76 130 135 140
 77 Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
 78 145 150 155 160
 79 Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
 80 165 170 175
 81 Lys Ala Glu Leu Ala Asp Ser Gln Ser
 82 180 185
 83 <210> SEQ ID NO 3
 84 <211> LENGTH: 3261
 85 <212> TYPE: DNA
 86 <213> ORGANISM: Homo sapiens
 87 <220> FEATURE:
 88 <221> NAME/KEY: CDS
 89 <222> LOCATION: (128)..(2440)
 90 <400> SEQUENCE: 3

91 taaaccaaga, agtttatcct caatcatctg gtatcaatat ataattttttt ttccttttttg 60
 92 ttactttta atgagatttg aggttgttct gtgattgtta tcagaattac catgcacaaa 120
 93 agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att 169
 94 Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile

All items 10 or
 even bunnies meet

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.